

SEQUENCE LISTING

<110> Viaxxel Biotech GmbH

<120> Compounds that affect CD83 expression, pharmaceutical compositions comprising said compounds and methods for identifying said compounds

<130> 84201

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<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(615)

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gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac 96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
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ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc 144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser

35

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45

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag 192
 Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
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gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt 240
 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
 65 70 75 80

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac 288
 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
 85 90 95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg 336
 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
 100 105 110

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga 384
 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
 115 120 125

tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag 432
 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
 130 135 140

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 Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
 145 150 155 160

ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct 528
 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
 165 170 175

aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag 576
 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
 180 185 190

cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga 618
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195 200 205

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<212> PRT
<213> Homo sapien

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35 40 45

Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
 50 55 60

Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
65 70 75 80

Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
85 90 95

Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
100 105 110

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
115 120 125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu

130 135 140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile

145 150 155 160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser

165 170 175

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys

180 185 190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val

195 200 205

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<221> CDS

<222> (14)..(601)

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Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala

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Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln

30 35 40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag 193
 Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
 45 50 55 60

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc 241
 Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
 65 70 75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc 289
 Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
 80 85 90

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac 337
 Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
 95 100 105

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct 385
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 Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
 125 130 135 140

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 Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
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 Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
 160 165 170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg 577
 Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
 175 180 185

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Thr Leu Pro Lys Thr Glu Thr Val

190 195

ccaagggcac atcagatcg tgtgcctgaa tgccacccgg acaagagaag aatgagctcc 691

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<212> PRT

<213> Mus musculus

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20	25	30
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Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala

35	40	45
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Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu

50	55	60
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Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala

65	70	75	80
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Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr

85

90

95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr

100

105

110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr

115

120

125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val

130

135

140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln

145

150

155

160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu

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Thr Glu Thr Val

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<213> Homo sapiens

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 Ile Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr
 20 25 30

cag gat gag tta cga agc ctg ttc agc agc att ggt gaa gtt gaa tct 144
 Gln Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser
 35 40 45

gca aaa ctt att cgg gat aaa gta gca gga cac agc ttg ggc tac ggc 192
 Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly
 50 55 60

ttt gtg aac tac gtg acc gcg aag gat gca gag aga gcg atc aac acg 240
 Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr
 65 70 75 80

ctg aac ggc ttg agg ctc cag tca aaa acc att aag gtg tcg tat gct 288
 Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala
 85 90 95

cgc ccg agc tca gag gtg atc aaa gac gcc aac ttg tac atc agc ggg 336
 Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly
 100 105 110

ctc ccg cgg acc atg acc cag aag gac gta gaa gac atg ttc tct cgg 384
 Leu Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg
 115 120 125

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 Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly
 130 135 140

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Leu Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala
 145 150 155 160

 gaa gag gca att acc agt ttc aat ggt cat aaa ccc cca ggt tcc tct 528
 Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser
 165 170 175

 gag ccc atc gca gtg aag ttt gca gcc aac ccc aac cag aac aaa aac 576
 Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn
 180 185 190

 gtg gca ctc ctc tcg cag ctg tac cac tcg cca gcg cga cggt ttc gga 624
 Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly
 195 200 205

 ggc ccc gtt cac cac cag gcg cag aga ttc agg ttc tcc ccc atg ggc 672
 Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly
 210 215 220

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 Val Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala
 225 230 235 240

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 Ser Ser Gly Trp Cys Ile Phe Ile Tyr Asn Leu Gly Gln Asp Ala Asp
 245 250 255

 gag ggg atc ctc tgg cag atg ttt ggg ccg ttt ggt gcc gtc acc aat 816
 Glu Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn
 260 265 270

 gtg aaa gtg atc cgc gac ttc aac acc aac aag tgc aaa ggg ttt ggc 864
 Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly
 275 280 285

 ttt gtg acc atg aca aac tat gaa gaa gcc gcg atg gcc ata gcc agc 912
 Phe Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser

290

295

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ctg aac ggc tac cgc ctg ggg gac aaa atc tta cag gtt tcc ttc aaa 960

Leu Asn Gly Tyr Arg Leu Gly Asp Lys Ile Leu Gln Val Ser Phe Lys

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315

320

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Thr Asn Lys Ser His Lys

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<213> Homo sapiens

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30

Gln Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser

35

40

45

Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly

50

55

60

Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr

65

70

75

80

Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala

85

90

95

Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly

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105

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Leu Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg

115

120

125

Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly

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135

140

Leu Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala

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150

155

160

Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser

165

170

175

Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn

180

185

190

Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly

195

200

205

Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly

210

215

220

Val Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala

225

230

235

240

Ser Ser Gly Trp Cys Ile Phe Ile Tyr Asn Leu Gly Gln Asp Ala Asp

245

250

255

Glu Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn

260

265

270

Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Gly Phe Gly

275

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285

Phe Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser

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Thr Asn Lys Ser His Lys
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<211> 42

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<212> DNA

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ggc cca acc acc ata aac aac aac tgt tcg tca cca gtt gac tct ggg 96
 Gly Pro Thr Thr Ile Asn Asn Asn Cys Ser Ser Pro Val Asp Ser Gly

20	25	30
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aac aca gaa gac agc aag acc aac tta ata gtc aac tac ctt cct cag 144
 Asn Thr Glu Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln

35	40	45
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aac atg aca cag gag gaa cta aag agt ctc ttt ggg agc att ggt gaa 192
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50	55	60
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 Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Gln Ser Leu

65	70	75	80
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 Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala

85	90	95
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100	105	110
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115	120	125
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10025357-421901

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 Val Ser Gly Leu Pro Lys Thr Met Thr Gln Lys Glu Leu Glu Gln Leu
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 Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln
 145 150 155 160

gtc act ggc ata tca agg ggt gta ggg ttt att cga ttt gac aag cga 528
 Val Thr Gly Ile Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg
 165 170 175

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 Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Pro
 180 185 190

ggt gcc acg gag cca atc act gta aag ttt gct aat aac cca agc caa 624
 Gly Ala Thr Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln
 195 200 205

aaa acc aat cag gcc atc ctt tcc cag ctg tac cag tct cca aac aga 672
 Lys Thr Asn Gln Ala Ile Leu Ser Gln Leu Tyr Gln Ser Pro Asn Arg
 210 215 220

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 Arg Tyr Pro Gly Pro Leu Ala Gln Gln Ala Gln Arg Phe Arg Leu Asp
 225 230 235 240

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 Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser Pro Met Thr
 245 250 255

att gac gga atg acc agt ttg gct gga att aat atc cct ggg cac cct 816
 Ile Asp Gly Met Thr Ser Leu Ala Gly Ile Asn Ile Pro Gly His Pro

260 265 270

gga aca ggg tgg tgt ata ttt gtg tac aac ctg gct cct gac gca gat 864
 Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu Ala Pro Asp Ala Asp

275 280 285

gag agt atc ctg tgg caa atg ttt ggg cct ttt gga gct gtc acc aat 912
 Glu Ser Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn
 290 295 300

gtg aag gtc atc cgt gac ttt aac acc aat aaa tgc aaa ggt ttt gga 960
 Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly
 305 310 315 320

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 Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Arg Ser
 325 330 335

ctc aat gga tac cgt ctg gga gac aga gta ctg cag gtc tcc ttt aag 1056
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 355

<210> 23

<211> 359

<212> PRT

<213> Homo sapiens

<400> 23

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35 40 45

Asn Met Thr Gln Glu Glu Leu Lys Ser Leu Phe Gly Ser Ile Gly Glu
50 55 60

Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Gln Ser Leu
65 70 75 80

Gly Tyr Gly Phe Val Asn Tyr Ile Asp Pro Lys Asp Ala Glu Lys Ala
85 90 95

Ile Asn Thr Leu Asn Gly Leu Arg Leu Gln Thr Lys Thr Ile Lys Val
100 105 110

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr
115 120 125

Val Ser Gly Leu Pro Lys Thr Met Thr Gln Lys Glu Leu Glu Gln Leu
130 135 140

Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln
145 150 155 160

Val Thr Gly Ile Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg
165 170 175

Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Pro
180 185 190

Gly Ala Thr Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln
195 200 205

Lys Thr Asn Gln Ala Ile Leu Ser Gln Leu Tyr Gln Ser Pro Asn Arg
210 215 220

Arg Tyr Pro Gly Pro Leu Ala Gln Gln Ala Gln Arg Phe Arg Leu Asp

225 230 235 240

Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser Pro Met Thr
245 250 255

Ile Asp Gly Met Thr Ser Leu Ala Gly Ile Asn Ile Pro Gly His Pro
260 265 270

Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu Ala Pro Asp Ala Asp
275 280 285

Glu Ser Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn
290 295 300

Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly
305 310 315 320

Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Arg Ser
325 330 335

Leu Asn Gly Tyr Arg Leu Gly Asp Arg Val Leu Gln Val Ser Phe Lys
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Thr Asn Lys Thr His Lys Ala
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<211> 1077

<212> DNA

<213> Homo sapiens

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 Pro Ala Gly Pro Ala Leu Pro Asn Gly Pro Leu Leu Gly Thr Asn Gly
 20 25 30

gcc act gac gac agc aag acc aac ctc atc gtc aac tac ctg ccc cag 144
 Ala Thr Asp Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln
 35 40 45

aac atg acc cag gat gag ttc aag agt ctc ttc ggc agc att ggc gac 192
 Asn Met Thr Gln Asp Glu Phe Lys Ser Leu Phe Gly Ser Ile Gly Asp
 50 55 60

atc gag tcc tgc aag ttg gtt cgg gac aag atc aca ggc aga gac ctt 240
 Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Arg Asp Leu
 65 70 75 80

ggc tac ggg ttt gtg aac tat cct gac ccc aat gat gca gac aaa gcc 288
 Gly Tyr Gly Phe Val Asn Tyr Pro Asp Pro Asn Asp Ala Asp Lys Ala
 85 90 95

atc aac acc ctc aac ggc ctc aaa tta cag acg aag acc atc aag gtg 336
 Ile Asn Thr Leu Asn Gly Leu Lys Leu Gln Thr Lys Thr Ile Lys Val
 100 105 110

tcc tat gcc aga ccc agt tca gca tcc atc cgg gat gct aac ctg tac 384
 Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr
 115 120 125

gtc agc ggg ctc ccc aag acc atg agc cag aaa gag atg gag cag ctc 432
 Val Ser Gly Leu Pro Lys Thr Met Ser Gln Lys Glu Met Glu Gln Leu
 130 135 140

ttc tcc cag tac ggc cgc atc atc acg tcc cgc atc ctg gtg gac cag 480
 Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln
 145 150 155 160

gtc aca ggt gtc tct cgg ggt gtg gga ttc atc cgc ttt gac aag agg 528
 Val Thr Gly Val Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg
 165 170 175

att gag gcc gaa gag gct atc aaa gga ctg aat ggg cag aag ccg ctg 576
 Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Leu
 180 185 190

ggc gca gct gag ccc atc aca gtc aag ttc gcg aac aac cca agt cag 624
 Gly Ala Ala Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln
 195 200 205

aag acg ggg cag gcg ctg ctc acc cac ctc tac cag tca tcc gcc cgg 672
 Lys Thr Gly Gln Ala Leu Leu Thr His Leu Tyr Gln Ser Ser Ala Arg
 210 215 220

cgc tac gca ggc ccc cta cac cat cag acc cag cgt ttc cgg ctg gac 720
 Arg Tyr Ala Gly Pro Leu His His Gln Thr Gln Arg Phe Arg Leu Asp
 225 230 235 240

aat ttg ctc aac atg gcc tac ggc gtc aag agg ttc tcg ccg atc gcc 768
 Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser Pro Ile Ala
 245 250 255

atc gat ggt atg agc ggc ctg gcg ggc gtg ggc ctg tcg ggg ggc gcg 816
 Ile Asp Gly Met Ser Gly Leu Ala Gly Val Gly Leu Ser Gly Gly Ala
 260 265 270

gcg ggc ggc tgg tgc atc ttc gtg tac aac ctg tca ccg gag gca gac 864
 Ala Gly Gly Trp Cys Ile Phe Val Tyr Asn Leu Ser Pro Glu Ala Asp
 275 280 285

gag agc gtg ctg tgg cag ctg ttc ggg cct ttt ggg gca gtc acc aac 912

Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe Gly Ala Val Thr Asn

290

295

300

gtc aag gtc atc cgt gat ttc acc acc aac aag tgc aag ggt ttc ggc 960

Val Lys Val Ile Arg Asp Phe Thr Thr Asn Lys Cys Lys Gly Phe Gly

305

310

315

320

tcc gtg acc atg acc aac tat gac gag gcg gcc atg gcc atc gcc agc 1008

Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Ala Ser

325

330

335

ctg aac ggc tat cgc ctg gcc gag cgc gtg ctg cag gtc tcc ttc aag 1056

Leu Asn Gly Tyr Arg Leu Ala Glu Arg Val Leu Gln Val Ser Phe Lys

340

345

350

acc agc aaa cag cac aag gcg 1077

Thr Ser Lys Gln His Lys Ala

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<212> PRT

<213> Homo sapiens

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Pro Ala Gly Pro Ala Leu Pro Asn Gly Pro Leu Leu Gly Thr Asn Gly

20

25

30

Ala Thr Asp Asp Ser Lys Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln

35

40

45

Asn Met Thr Gln Asp Glu Phe Lys Ser Leu Phe Gly Ser Ile Gly Asp

50

55

60

Ile Glu Ser Cys Lys Leu Val Arg Asp Lys Ile Thr Gly Arg Asp Leu
 65 70 75 80

Gly Tyr Gly Phe Val Asn Tyr Pro Asp Pro Asn Asp Ala Asp Lys Ala
 85 90 95

Ile Asn Thr Leu Asn Gly Leu Lys Leu Gln Thr Lys Thr Ile Lys Val
 100 105 110

Ser Tyr Ala Arg Pro Ser Ser Ala Ser Ile Arg Asp Ala Asn Leu Tyr
 115 120 125

Val Ser Gly Leu Pro Lys Thr Met Ser Gln Lys Glu Met Glu Gln Leu
 130 135 140

Phe Ser Gln Tyr Gly Arg Ile Ile Thr Ser Arg Ile Leu Val Asp Gln
 145 150 155 160

Val Thr Gly Val Ser Arg Gly Val Gly Phe Ile Arg Phe Asp Lys Arg
 165 170 175

Ile Glu Ala Glu Glu Ala Ile Lys Gly Leu Asn Gly Gln Lys Pro Leu
 180 185 190

Gly Ala Ala Glu Pro Ile Thr Val Lys Phe Ala Asn Asn Pro Ser Gln
 195 200 205

Lys Thr Gly Gln Ala Leu Leu Thr His Leu Tyr Gln Ser Ser Ala Arg
 210 215 220

Arg Tyr Ala Gly Pro Leu His His Gln Thr Gln Arg Phe Arg Leu Asp
 225 230 235 240

Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser Pro Ile Ala
 245 250 255

10025367-200001

Ile Asp Gly Met Ser Gly Leu Ala Gly Val Gly Leu Ser Gly Gly Ala

260

265

270

Ala Gly Gly Trp Cys Ile Phe Val Tyr Asn Leu Ser Pro Glu Ala Asp

275

280

285

Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe Gly Ala Val Thr Asn

290

295

300

Val Lys Val Ile Arg Asp Phe Thr Thr Asn Lys Cys Lys Gly Phe Gly

305

310

315

320

Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala Met Ala Ile Ala Ser

325

330

335

Leu Asn Gly Tyr Arg Leu Ala Glu Arg Val Leu Gln Val Ser Phe Lys

340

345

350

Thr Ser Lys Gln His Lys Ala

355

<210> 26

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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Met Val Met Ile Ile Ser Thr Met Glu Pro Gln Val Ser Asn Gly Pro

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10

15

aca tcc aat aca agc aat gga ccc tcc agc aac aac aga aac tgt cct 96
 Thr Ser Asn Thr Ser Asn Gly Pro Ser Ser Asn Asn Arg Asn Cys Pro

20 25 30

tct ccc atg caa aca ggg gca acc aca gat gac agc aaa acc aac ctc 144
 Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu
 35 40 45

atc gtc aac tat tta ccc cag aat atg acc caa gaa gaa ttc agg agt 192
 Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser
 50 55 60

ctc ttc ggg agc att ggt gaa ata gaa tcc tgc aaa ctt gtg aga gac 240
 Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp
 65 70 75 80

aaa att aca gga cag agt tta ggg tat gga ttt gtt aac tat att gat 288
 Lys Ile Thr Gly Gln Ser Leu Gly Tyr Gly Phe Val Asn Tyr Ile Asp
 85 90 95

cca aag gat gca gag aaa gcc atc aac act tta aat gga ctc aga ctc 336
 Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu
 100 105 110

cag acc aaa acc ata aag gtc tca tat gcc cgt ccg agc tct gcc tca 384
 Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser
 115 120 125

atc agg gat gct aac ctc tat gtt agc ggc ctt ccc aaa acc atg acc 432
 Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr
 130 135 140

cag aag gaa ctg gag caa ctt ttc tcg caa tac ggc cgt atc atc acc 480
 Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr
 145 150 155 160

tca cga atc ctg gtt gat caa gtc aca gga gtg tcc aga ggg gtg gga 528

Ser Arg Ile Leu Val Asp Gln Val Thr Gly Val Ser Arg Gly Val Gly

165 170 175

ttc atc cgc ttt gat aag agg att gag gca gaa gaa gcc atc aaa ggg 576

Phe Ile Arg Phe Asp Lys Arg Ile Glu Ala Glu Glu Ala Ile Lys Gly

180 185 190

ctg aat ggc cag aag ccc agc ggt gct acg gaa ccg att act gtg aag 624

Leu Asn Gly Gln Lys Pro Ser Gly Ala Thr Glu Pro Ile Thr Val Lys

195 200 205

ttt gcc aac aac ccc agc cag aag tcc agc cag gcc ctg ctc tcc cag 672

Phe Ala Asn Asn Pro Ser Gln Lys Ser Ser Gln Ala Leu Leu Ser Gln

210 215 220

ctc tac cag tcc cct aac cgg cgc tac cca ggt cca ctt cac cac cag 720

Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln

225 230 235 240

gct cag agg ttc agg ctg gac aat ttg ctt aat atg gcc tat ggc gta 768

Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val

245 250 255

aag aga ctg atg tct gga cca gtc ccc cct tct gct tgt tcc ccc agg 816

Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg

260 265 270

ttc tcc cca att acc att gat gga atg aca agc ctt gtg gga atg aac 864

Phe Ser Pro Ile Thr Ile Asp Gly Met Thr Ser Leu Val Gly Met Asn

275 280 285

atc cct ggt cac aca gga act ggg tgg tgc atc ttt gtc tac aac ctg 912

Ile Pro Gly His Thr Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu

290 295 300

tcc ccc gat tcc gat gag agt gtc ctc tgg cag ctc ttt ggc ccc ttt 960

Ser Pro Asp Ser Asp Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe

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gga gca gtg aac aac gta aag gtg att cgt gac ttc aac acc aac aag 1008			
Gly Ala Val Asn Asn Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys			
325	330	335	
tgc aag gga ttc ggc ttt gtc acc atg acc aac tat gat gag gcg gcc 1056			
Cys Lys Gly Phe Gly Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala			
340	345	350	
atg gcc atc gcc agc ctc aac ggg tac cgc ctg gga gac aga gtg ttg 1104			
Met Ala Ile Ala Ser Leu Asn Gly Tyr Arg Leu Gly Asp Arg Val Leu			
355	360	365	
caa gtt tcc ttt aaa acc aac aaa gcc cac aag tcc 1140			
Gln Val Ser Phe Lys Thr Asn Lys Ala His Lys Ser			
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Ser Pro Met Gln Thr Gly Ala Thr Thr Asp Asp Ser Lys Thr Asn Leu			
35	40	45	
Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln Glu Glu Phe Arg Ser			
50	55	60	

Leu Phe Gly Ser Ile Gly Glu Ile Glu Ser Cys Lys Leu Val Arg Asp
65 70 75 80

Lys Ile Thr Gly Gln Ser Leu Gly Tyr Gly Phe Val Asn Tyr Ile Asp
85 90 95

Pro Lys Asp Ala Glu Lys Ala Ile Asn Thr Leu Asn Gly Leu Arg Leu
100 105 110

Gln Thr Lys Thr Ile Lys Val Ser Tyr Ala Arg Pro Ser Ser Ala Ser
115 120 125

Ile Arg Asp Ala Asn Leu Tyr Val Ser Gly Leu Pro Lys Thr Met Thr
130 135 140

Gln Lys Glu Leu Glu Gln Leu Phe Ser Gln Tyr Gly Arg Ile Ile Thr
145 150 155 160

Ser Arg Ile Leu Val Asp Gln Val Thr Gly Val Ser Arg Gly Val Gly
165 170 175

Phe Ile Arg Phe Asp Lys Arg Ile Glu Ala Glu Glu Ala Ile Lys Gly
180 185 190

Leu Asn Gly Gln Lys Pro Ser Gly Ala Thr Glu Pro Ile Thr Val Lys
195 200 205

Phe Ala Asn Asn Pro Ser Gln Lys Ser Ser Gln Ala Leu Leu Ser Gln
210 215 220

Leu Tyr Gln Ser Pro Asn Arg Arg Tyr Pro Gly Pro Leu His His Gln
225 230 235 240

Ala Gln Arg Phe Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val
245 250 255

Lys Arg Leu Met Ser Gly Pro Val Pro Pro Ser Ala Cys Ser Pro Arg

260

265

270

Phe Ser Pro Ile Thr Ile Asp Gly Met Thr Ser Leu Val Gly Met Asn

275

280

285

Ile Pro Gly His Thr Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu

290

295

300

Ser Pro Asp Ser Asp Glu Ser Val Leu Trp Gln Leu Phe Gly Pro Phe

305

310

315

320

Gly Ala Val Asn Asn Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys

325

330

335

Cys Lys Gly Phe Gly Phe Val Thr Met Thr Asn Tyr Asp Glu Ala Ala

340

345

350

Met Ala Ile Ala Ser Leu Asn Gly Tyr Arg Leu Gly Asp Arg Val Leu

355

360

365

Gln Val Ser Phe Lys Thr Asn Lys Ala His Lys Ser

370

375

380